

Please replace the paragraph under the heading entitled "Cross-References to Related Applications" on page 1, line 11, with the following rewritten paragraph (see earlier amendment to this section made in the preliminary amendment filed August 1, 2001):

This application is a divisional of U.S. Patent Application No. 09/686,020, filed October 10, 2000, which claims benefit of U.S. Provisional Patent Application 60/159,015, filed October 12, 1999, and U.S. Provisional Patent Application 60/159,210, filed October 13, 1999, and U.S. Provisional Patent Application 60/172,979, filed December 20, 1999, and U.S. Provisional Patent Application 60/173,388, filed December 28, 1999, and U.S. Provisional Patent Application 60/186,626, filed March 3, 2000. The disclosure of each of the aforementioned applications is expressly incorporated herein by reference in its entirety and for all purposes.

Please insert the following heading and paragraph after the section entitled "Cross-Reference to Related Applications" and before the section entitled "Background of the Invention" on page 1:

Field Of The Invention

The invention relates to a human chemokine receptor, and to compositions and methods useful for diagnosing and treating physiologic and pathologic conditions mediated by the receptor and its ligand. The invention finds application in the biomedical sciences.

Please replace the paragraph beginning at page 13, line 27, with the following rewritten paragraph:

One example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence,

which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a wordlength (W) of 11, the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

Please replace the paragraph beginning at page 51, line 15, with the following rewritten paragraph:

Chemokines are well known in the art. Exemplary chemokines include those listed in Fig. 4(a) and homologs in other species (e.g., mammalian, mouse, rat rabbit, human, non-human primate, and the like. The following references describe certain cytokines. Additional references describing these and other chemokines known in the art are provided in the R&D Systems Catalog (1999) and (2000) R&D Systems Inc., 614 McKinley Place N.E. MN 55413, the R&D online catalog at www.rndsystems.com (e.g., October 10, 1999), both of which are incorporated by reference for all purposes, the CFB (Cytokine Facts Book, 1994, Academic Press Ltd.), Chemokine Facts Book, 1997, Academic Press Ltd., incorporated by reference for all purposes, and the GenBank protein sequence database.

Please replace the paragraph beginning at page 53, line 21, with the following rewritten paragraph: